

M. HINES



RAW SEQUENCE LISTING

DATE: 08/06/2003

PATENT APPLICATION: US/09/876,813

TIME: 08:52:43

Input Set : N:\Crf3\RULE60\09876813.raw.txt

Output Set: N:\CRF4\08062003\I876813.raw

```

1 <110> APPLICANT: Gilbert, Teresa
2      Hart, Charles E.
3      Sheppard, Paul O.
4 <120> TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
5 <130> FILE REFERENCE: 99-19
6 <140> CURRENT APPLICATION NUMBER: 09/876,813
7 <141> CURRENT FILING DATE: 2001-06-06
9 <150> PRIOR APPLICATION NUMBER: US/09/564,595
10 <151> PRIOR FILING DATE: 2000-05-03
12 <150> PRIOR APPLICATION NUMBER: US 09/304,216
13 <151> PRIOR FILING DATE: 1999-05-03
14 <150> PRIOR APPLICATION NUMBER: US 60/164,463
15 <151> PRIOR FILING DATE: 1999-11-10
16 <150> PRIOR APPLICATION NUMBER: US 60/180,169
17 <151> PRIOR FILING DATE: 2000-02-04
18 <160> NUMBER OF SEQ ID NOS: 57
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1882
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (226)...(1338)
28 <400> SEQUENCE: 1
29      ccgtcaccat ttatcagctc agcaccacaa ggaagtgcgg caccacacacg cgctcggaaa      60
30      gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg      120
31      cagggcgagc gcaggcgggc agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac      180
32      ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc      237
33                                     Met His Arg Leu
34                                     1
35      atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac      285
36      Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
37      5          10          15          20
38      act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc      333
39      Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
40      25          30          35
41      aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga      381
42      Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
43      40          45          50
44      gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga      429
45      Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
46      55          60          65

```

ENTERED

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47	ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac	477
48	Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His	
49	70 75 80	
50	tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga	525
51	Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	
52	85 90 95 100	
53	tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt	573
54	Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	
55	105 110 115	
56	gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga	621
57	Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	
58	120 125 130	
59	cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
60	His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
61	135 140 145	
62	atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
63	Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
64	150 155 160	
65	att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765
66	Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	
67	165 170 175 180	
68	acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813
69	Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	
70	185 190 195	
71	tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861
72	Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	
73	200 205 210	
74	aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909
75	Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn	
76	215 220 225	
77	cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957
78	Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro	
79	230 235 240	
80	cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005
81	Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu	
82	245 250 255 260	
83	gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053
84	Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn	
85	265 270 275	
86	tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101
87	Tyr Ser Val Asn Ile Arg Glu Glu Lys Leu Ala Asn Val Val Phe	
88	280 285 290	
89	ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149
90	Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys	
91	295 300 305	
92	gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg	1197
93	Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val	
94	310 315 320	
95	aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg	1245

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```

96   Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
97   325                               330                               335                               340
98   agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac      1293
99   Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
100                                345                                350                                355
101   cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa      1338
102   His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
103                                360                                365                                370
104   gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat      1398
105   aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca      1458
106   agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca      1518
107   tcaacttcta taccctaagaa tataggattg catttaataa tagtgtttga gggtatatat      1578
108   gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt      1638
109   ttttgggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa      1698
110   tcctttgccca aaataaggga tgggtcaaata tatgaaacat gtcttttagaa aatttaggag      1758
111   ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa      1818
112   agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat      1878
113   tatt                                                                1882
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 370
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
120   Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
121   1                               5                               10                               15
122   Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
123   20                               25                               30
124   Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
125   35                               40                               45
126   Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
127   50                               55                               60
128   Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
129   65                               70                               75                               80
130   Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
131   85                               90                               95
132   Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
133   100                              105                              110
134   Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
135   115                              120                              125
136   Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
137   130                              135                              140
138   Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
139   145                              150                              155                              160
140   Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
141   165                              170                              175
142   Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
143   180                              185                              190
144   Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
145   195                              200                              205

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Output Set: N:\CRF4\08062003\I876813.raw

```

146   Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
147       210               215               220
148   Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
149       225               230               235               240
150   Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
151       245               250               255
152   Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
153       260               265               270
154   Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
155       275               280               285
156   Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
157       290               295               300
158   Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
159       305               310               315               320
160   Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
161       325               330               335
162   His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
163       340               345               350
164   Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
165       355               360               365
166   Pro Arg
167       370

```

169 <210> SEQ ID NO: 3

170 <211> LENGTH: 126

171 <212> TYPE: PRT

172 <213> ORGANISM: Artificial Sequence

173 <220> FEATURE:

174 <223> OTHER INFORMATION: polypeptide motif

W--> 175 <221> NAME/KEY: VARIANT

176 <222> LOCATION: (2)...(19)

177 <223> OTHER INFORMATION: Xaa = Any Amino Acid

W--> 178 <221> VARIANT

179 <222> LOCATION: (20)...(34)

180 <223> OTHER INFORMATION: Xaa = Any Amino Acid or is not present

W--> 181 <221> VARIANT

182 <222> LOCATION: (36)...(45)

183 <223> OTHER INFORMATION: Xaa = Any Amino Acid

W--> 184 <221> VARIANT

185 <222> LOCATION: (46)...(72)

186 <223> OTHER INFORMATION: Xaa = Any Amino Acid or is not present

W--> 187 <221> VARIANT

188 <222> LOCATION: (74)...(93)

189 <223> OTHER INFORMATION: Xaa = Any Amino Acid

W--> 190 <221> VARIANT

191 <222> LOCATION: (94)...(123)

192 <223> OTHER INFORMATION: Xaa = Any Amino Acid or is not present

W--> 193 <221> VARIANT

194 <222> LOCATION: (125)...(125)

195 <223> OTHER INFORMATION: Xaa = Any Amino Acid

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Input Set : N:\Crf3\RULE60\09876813.raw.txt

Output Set: N:\CRF4\08062003\I876813.raw

```

W--> 196 <400> 3
W--> 197   Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
198       1           5           10           15
199   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
200           20           25           30
201   Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
202           35           40           45
203   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
204       50           55           60
205   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
206       65           70           75           80
207   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
208           85           90           95
209   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210           100          105          110
211   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys
212           115          120          125
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 24
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: polypeptide motif
W--> 220 <221> NAME/KEY: VARIANT
221 <222> LOCATION: (2)...(2)
222 <223> OTHER INFORMATION: Xaa = Lys or Arg
W--> 223 <221> VARIANT
224 <222> LOCATION: (4)...(4)
225 <223> OTHER INFORMATION: Xaa = Asp, Asn or Glu
W--> 226 <221> VARIANT
227 <222> LOCATION: (5)...(5)
228 <223> OTHER INFORMATION: Xaa = Trp, Tyr or Phe
W--> 229 <221> VARIANT
230 <222> LOCATION: (6)...(16)
231 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 232 <221> VARIANT
233 <222> LOCATION: (17)...(20)
234 <223> OTHER INFORMATION: Xaa = Any Amino Acid or is not present
W--> 235 <221> VARIANT
236 <222> LOCATION: (22)...(22)
237 <223> OTHER INFORMATION: Xaa = Lys or Arg
W--> 238 <221> VARIANT
239 <222> LOCATION: (23)...(23)
240 <223> OTHER INFORMATION: Xaa = Trp, Tyr or Phe
W--> 241 <400> 4
W--> 242   Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
243       1           5           10           15
244   Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys
245           20

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\Cr3\RULE60\09876813.raw.txt
Output Set: N:\CRF4\08062003\I876813.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:3; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,36,38,40,41,42,43,44,45
Seq#:3; Xaa Pos. 46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64
Seq#:3; Xaa Pos. 65,66,67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,84
Seq#:3; Xaa Pos. 85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:3; Xaa Pos. 103,104,105,106,107,108,109,110,111,112,113,114,115,116
Seq#:3; Xaa Pos. 117,118,119,120,121,122,123,125
Seq#:4; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23
Seq#:6; N Pos. 9,12,21,27,30,39,51,57,63,66,69,72,75,81,84,87,96,99,102,108
Seq#:6; N Pos. 114,117,120,129,138,141,147,153,156,165,174,180,186,192,198
Seq#:6; N Pos. 201,204,210,216,222,225,231,234,237,240,246,249,255,267,270
Seq#:6; N Pos. 279,282,300,303,312,330,342,348,360,366,369,372,381,384,387
Seq#:6; N Pos. 396,408,411,414,417,426,429,432,450,459,474,477,483,486,504
Seq#:6; N Pos. 507,510,525,528,531,534,537,543,555,558,561,564,567,573,576
Seq#:6; N Pos. 579,582,591,594,597,600,603,609,612,615,621,627,630,645,657
Seq#:6; N Pos. 660,669,672,687,693,708,723,729,732,735,741,744,747,750,762
Seq#:6; N Pos. 768,774,780,786,789,801,807,813,819,822,825,834,837,846,855
Seq#:6; N Pos. 861,864,870,873,882,885,891,894,897,903,909,912,921,927,930
Seq#:6; N Pos. 933,942,945,951,960,963,969,972,990,993,1005,1008,1020,1023
Seq#:6; N Pos. 1026,1029,1032,1038,1044,1047,1050,1062,1077,1095,1098,1101
Seq#:6; N Pos. 1104,1107,1110
Seq#:7; N Pos. 3,9,12
Seq#:8; N Pos. 3,9,12
Seq#:9; N Pos. 6,9,15
Seq#:10; N Pos. 9,12
Seq#:11; N Pos. 1,3,6,9,10,12
Seq#:12; N Pos. 6,8,9,12,15,17
Seq#:13; N Pos. 9
Seq#:14; N Pos. 4,5,6,7,9,15
Seq#:15; N Pos. 3,9,11,12,13,14
Seq#:16; N Pos. 6,9,12
Seq#:17; N Pos. 5,6,9,12,15
Seq#:18; N Pos. 3,6,9,12,13
Seq#:19; N Pos. 1,13
Seq#:20; N Pos. 1,13
Seq#:21; N Pos. 2,8,11,14
Seq#:22; N Pos. 2,8,11,14
Seq#:23; N Pos. 2,5,8,11
Seq#:24; N Pos. 2,5,8,11

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09876813.raw.txt

Output Set: N:\CRF4\08062003\I876813.raw

L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:178 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:187 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:193 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:220 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:223 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:229 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:232 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:238 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:241 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:263 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:266 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
L:293 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:296 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:305 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:308 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:317 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:329 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:332 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:341 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:344 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:353 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:365 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:368 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:377 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09876813.raw.txt

Output Set: N:\CRF4\08062003\I876813.raw

L:389 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:392 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:401 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:404 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:413 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:416 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:425 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:428 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:437 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:440 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:449 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:452 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:461 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:464 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:473 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:476 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:485 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:488 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:497 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:500 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0